

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/569,076
Source: 1 FWP
Date Processed by STIC: 3/2/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 03/02/2006

PATENT APPLICATION: US/10/569,076

TIME: 10:28:51

Input Set : A:\SEQlist003.txt

Output Set: N:\CRF4\03022006\J569076.raw

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7 <110> APPLICANT: BERDEL, Wolfgang E.
8     MESTERS, Rolf M.
10 <120> TITLE OF INVENTION: Fusion polypeptides for antivasular tumor therapy
12 <130> FILE REFERENCE: 20490.003
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/569,076
C--> 14 <141> CURRENT FILING DATE: 2006-02-21
14 <150> PRIOR APPLICATION NUMBER: PCT/EP04/009364
15 <151> PRIOR FILING DATE: 2004-08-20
17 <150> PRIOR APPLICATION NUMBER: DE 10338733.1
18 <151> PRIOR FILING DATE: 2003-08-22
20 <160> NUMBER OF SEQ ID NOS: 41
22 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 263
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
W--> 31 <221> NAME/KEY: Amino acid sequence of human TF
33 <400> SEQUENCE: 1
34 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
35 1          5          10          15
37 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
38          20          25          30
40 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
41          35          40          45
43 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
44          50          55          60
46 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
47 65          70          75          80
49 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
50          85          90          95
52 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
53          100         105         110
55 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
56          115         120         125
58 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
59          130         135         140
61 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
62 145         150         155         160
64 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
65          165         170         175
67 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
68          180         185         190

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70 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 71 195 200 205
 73 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile
 74 210 215 220
 76 Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile
 77 225 230 235 240
 79 Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu
 80 245 250 255

82 Asn Ser Pro Leu Asn Val Ser

83 260

88 <210> SEQ ID NO: 2

89 <211> LENGTH: 218

90 <212> TYPE: PRT

91 <213> ORGANISM: Homo sapiens

93 <220> FEATURE:

W--> 94 <221> NAME/KEY: Amino acid sequence of tTF1-218

96 <400> SEQUENCE: 2

97 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 98 1 5 10 15

100 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 101 20 25 30

103 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 104 35 40 45

106 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 107 50 55 60

109 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 110 65 70 75 80

112 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 113 85 90 95

115 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
 116 100 105 110

118 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
 119 115 120 125

121 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
 122 130 135 140

124 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
 125 145 150 155 160

127 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
 128 165 170 175

130 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
 131 180 185 190

133 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 134 195 200 205

136 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg
 137 210 215

141 <210> SEQ ID NO: 3

142 <211> LENGTH: 224

143 <212> TYPE: PRT

144 <213> ORGANISM: Artificial

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Input Set : A:\SEQlist003.txt

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146 <220> FEATURE:

W--> 147 <221> NAME/KEY: Amino acid sequence of tTF-GRGDSP

148 <223> OTHER INFORMATION: Synthetic construct

150 <400> SEQUENCE: 3

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151 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
152 1          5          10          15
154 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
155          20          25          30
157 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
158          35          40          45
160 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
161          50          55          60
163 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
164 65          70          75          80
166 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
167          85          90          95
169 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
170          100         105         110
172 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
173          115         120         125
175 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
176          130         135         140
178 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
179 145          150         155         160
181 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
182          165         170         175
184 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
185          180         185         190
187 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
188          195         200         205
190 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Arg Gly Asp Ser Asp
191          210         215         220

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196 <210> SEQ ID NO: 4

197 <211> LENGTH: 225

198 <212> TYPE: PRT

199 <213> ORGANISM: Artificial

201 <220> FEATURE:

W--> 202 <221> NAME/KEY: Amino acid sequence of tTF-GNGRAHA

203 <223> OTHER INFORMATION: Synthetic construct

205 <400> SEQUENCE: 4

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206 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
207 1          5          10          15
209 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
210          20          25          30
212 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
213          35          40          45
215 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
216          50          55          60
218 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala

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219 65          70          75          80
221 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
222          85          90          95
224 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
225          100          105          110
227 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
228          115          120          125
230 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
231          130          135          140
233 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
234 145          150          155          160
236 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
237          165          170          175
239 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
240          180          185          190
242 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
243          195          200          205
245 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Asn Gly Arg Ala His
246 210          215          220
248 Ala
249 225

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256 <210> SEQ ID NO: 5

257 <211> LENGTH: 228

258 <212> TYPE: PRT

259 <213> ORGANISM: Artificial

261 <220> FEATURE:

W--> 262 <221> NAME/KEY: Amino acid sequence of tTF-GALNGRSHAG

263 <223> OTHER INFORMATION: Synthetic construct

265 <400> SEQUENCE: 5

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266 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
267 1          5          10          15
269 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
270          20          25          30
272 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
273          35          40          45
275 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
276          50          55          60
278 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
279 65          70          75          80
281 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
282          85          90          95
284 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
285          100          105          110
287 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
288          115          120          125
290 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
291          130          135          140
293 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
294 145          150          155          160

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Input Set : A:\SEQlist003.txt

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296 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
297           165           170           175
299 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
300           180           185           190
302 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
303           195           200           205
305 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Ala Leu Asn Gly Arg
306           210           215           220
308 Ser His Ala Gly
309 225

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314 <210> SEQ ID NO: 6

315 <211> LENGTH: 225

316 <212> TYPE: PRT

317 <213> ORGANISM: Artificial

319 <220> FEATURE:

W--> 320 <221> NAME/KEY: Amino acid sequence of tTF-GCNGRCG

321 <223> OTHER INFORMATION: Synthetic construct

323 <400> SEQUENCE: 6

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324 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
325 1           5           10           15
327 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
328           20           25           30
330 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
331           35           40           45
333 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
334           50           55           60
336 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
337 65           70           75           80
339 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
340           85           90           95
342 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
343           100          105          110
345 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
346           115          120          125
348 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
349           130          135          140
351 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
352 145          150          155          160
354 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
355           165          170          175
357 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
358           180          185          190
360 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
361           195          200          205
363 Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Gly Cys Asn Gly Arg Cys
364           210          215          220
366 Gly
367 225
374 <210> SEQ ID NO: 7

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/02/2006
PATENT APPLICATION: US/10/569,076 TIME: 10:28:52

Input Set : A:\SEQlist003.txt
Output Set: N:\CRF4\03022006\J569076.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,10,11,12,13,14,15,18,19,20,21,22,23,24,25,26,27,28,29,30,31

Seq#:32,33,34,35,36,37,38,39,40,41

VERIFICATION SUMMARY

DATE: 03/02/2006

PATENT APPLICATION: US/10/569,076

TIME: 10:28:52

Input Set : A:\SEQlist003.txt

Output Set: N:\CRF4\03022006\J569076.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:262 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:320 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:380 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:440 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:498 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:501 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:536 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:572 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:609 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:646 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:681 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:716 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:749 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:751 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:762 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:765 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:779 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:807 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:820 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:834 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:848 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:864 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
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L:893 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:907 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:921 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:935 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:953 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:973 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:1036 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:1141 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:1156 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:1172 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38